SEQUENCE LISTING

(1) GENERAL INFORMATION:

   (i) APPLICANT: Lobb, Roy R.

  (ii) TITLE OF INVENTION: Treatment For Inflammatory Bowel Disease

 (iii) NUMBER OF SEQUENCES: 4

  (iv) CORRESPONDENCE ADDRESS:
     (A) ADDRESSEE: LAHIVE & COCKFIELD
     (B) STREET: 60 State Street, Suite 510
     (C) CITY: Boston
     (D) STATE: Massachusetts
     (E) COUNTRY: USA
     (F) ZIP: 02109-1875

   (v) COMPUTER READABLE FORM:
     (A) MEDIUM TYPE: Floppy disk
     (B) COMPUTER: IBM PC compatible
     (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

  (vi) CURRENT APPLICATION DATA:
     (A) APPLICATION NUMBER: US 08/373,857
     (B) FILING DATE: 18-JAN-1995
     (C) CLASSIFICATION:

 (vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: US 08/284,603
     (B) FILING DATE: 11-AUG-1994
     (C) CLASSIFICATION:

 (vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: US 07/835,139
     (B) FILING DATE: 12-FEB-1992
     (C) CLASSIFICATION:

 (vii) PRIOR APPLICATION DATA:
     (A) APPLICATION NUMBER: PCT/US93/00924
     (B) FILING DATE: 02-FEB-1993

 (viii) ATTORNEY/AGENT INFORMATION:
     (A) NAME: Louis Myers (PLM)
     (B) REGISTRATION NUMBER: 35,965
     (C) REFERENCE/DOCKET NUMBER: BGP-031USCP

  (ix) TELECOMMUNICATION INFORMATION:
     (A) TELEPHONE: (617)227-7400
     (B) TELEFAX: (617)227-5941

(2) INFORMATION FOR SEQ ID NO:1:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 360 base pairs
     (B) TYPE: nucleic acid

```
        (C)  STRANDEDNESS: single
        (D)  TOPOLOGY: linear

    (ii)  MOLECULE TYPE: cDNA


    (ix)  FEATURE:
        (A)  NAME/KEY: CDS
        (B)  LOCATION: 1..360

    (ix)  FEATURE:
        (A)  NAME/KEY: misc_feature
        (B)  LOCATION: 1
        (D)  OTHER INFORMATION: /note= "pBAG159 insert:
             HP1/2 heavy vhain variable region; amino acid 1 is
             Glu (E) but Gln (Q) may be substituted"


    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:1:
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GTC AAA CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC TCA        48
Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
 1               5                   10                  15

GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC TAT        96
Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
             20                  25                  30

ATG CAC TGG GTG AAG CAG AGG CCT GAA CAG GGC CTG GAG TGG ATT GGA       144
Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
         35                  40                  45

AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC CAG       192
Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
     50                  55                  60

GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG CTG       240
Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
 65                  70                  75                  80

CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT GCA       288
Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
             85                  90                  95

GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC CAA       336
Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
         100                 105                 110

GGG ACC ACG GTC ACC GTC TCC TCA                                       360
Gly Thr Thr Val Thr Val Ser Ser
         115                 120
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(2) INFORMATION FOR SEQ ID NO:2:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 120 amino acids
             (B) TYPE: amino acid

(D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: protein

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
 1   5   10   15

Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
                    20   25   30

Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
                35   40   45

Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
          50   55   60

Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
 65   70   75   80

Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
                    85   90   95

Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
                100   105   110

Gly Thr Thr Val Thr Val Ser Ser
                115   120

(2) INFORMATION FOR SEQ ID NO:3:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 318 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: cDNA

          (ix) FEATURE:
               (A) NAME/KEY: CDS
               (B) LOCATION: 1..318
               (D) OTHER INFORMATION: /product= "HP1/2 light
                    chain variable region"

          (ix) FEATURE:
               (A) NAME/KEY: misc_feature
               (B) LOCATION: 1
               (D) OTHER INFORMATION: /note= "pBAG172 insert:
                    HP1/2 light chain variable region"

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT ATT GTG ATG ACC CAG ACT CCC AAA TTC CTG CTT GTT TCA GCA GGA   48
Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly

GAC AGG GTT ACC ATA ACC TGC AAG GCC AGT CAG AGT GTG ACT AAT GAT   96
Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
            20   25   30

GTA GCT TGG TAC CAA CAG AAG CCA GGG CAG TCT CCT AAA CTG CTG ATA   144
Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
            35   40   45

TAT TAT GCA TCC AAT CGC TAC ACT GGA GTC CCT GAT CGC TTC ACT GGC   192
Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
            50   55   60

AGT GGA TAT GGG ACG GAT TTC ACT TTC ACC ATC AGC ACT GTG CAG GCT   240
Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
65   70   75   80

GAA GAC CTG GCA GTT TAT TTC TGT CAG CAG GAT TAT AGC TCT CCG TAC   288
Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
            85   90   95

ACG TTC GGA GGG GGG ACC AAG CTG GAG ATC   318
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100   105

(2) INFORMATION FOR SEQ ID NO:4:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 106 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser Ile Val Met Thr Gln Thr Pro Lys Phe Leu Leu Val Ser Ala Gly
 1   5   10   15

Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Ser Val Thr Asn Asp
            20   25   30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
            35   40   45

Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
            50   55   60

Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
65   70   75   80

Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
            85   90   95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
            100   105